

Objective scoring of psoriasis area and severity index in 2D RGB images using deep learning

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Abstract

Psoriasis Severity and Area Index (PASI) is a gold standard scoring system for the assessment of Psoriasis skin disease. Generally, PASI scoring is done manually by expert dermatologists through visual and touch senses for psoriasis diagnosis and their treatment's validation. This subjective approach raises several limitations and becomes unreliable. Many conventional and machine learning-based works are proposed for objective estimation of psoriasis area and severity from 2D RGB images. However, these works are validated on small datasets, require manual pre-processing, and rely heavily on hand-crafted features. In the proposed work, a fully automated system based on deep learning is designed for automated PASI scoring from raw 2D RGB images. This system contains a segmentation and three classification models for objective estimation of psoriasis area and severity scores for all three clinical symptoms of psoriasis, respectively. The psoriasis area is estimated by segmenting healthy and unhealthy regions simultaneously using a lightweight network as a backbone with UNet. After segmentation, the severity scores for each segmented lesion are automatically estimated by using a hybrid classification model. This model is developed by adopting a lightweight network for local feature extraction and integrating it with a vision transformer for learning global features. The psoriasis dataset used in the proposed work is self-prepared and contains 1,018 photographic images from different body regions of 212 psoriasis patients. The exhaustive performance analysis is done for the automatic estimation of each parameter of PASI. The proposed work achieves mean absolute error of 0.04, 0.23, 0.22, and 0.21 for objective estimation of Area, Redness, Scaliness, and Thickness scores, respectively. The mean absolute error obtained by the proposed system for automatic scoring of PASI is 1.02. The comparative studies with existing works further validate the efficacy of the proposed work. This work can further be improvised by using data from multi-centre and regions in a large population.

Keywords Psoriasis · Lesion segmentation · Severity classification · PASI · Deep learning · Vision transformer

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1 Introduction

Psoriasis is a chronic, complex, autoimmune, and inflammatory skin disease affecting about 1–3% of the world's population [1]. In psoriasis, skin cells grow more expeditious than in healthy human beings. For a healthy person, the development phase of skin cells is 28 to 30 days while it takes only 3 to 4 days in psoriasis patients [2]. It manifests as red, dry, itchy, raised, and scaly patches in the human skin. It generally occurs on the knees, scalp, elbows, and trunk, and further spreads to different parts of the body. It can develop in any human being regardless of age, gender, and community [3]. There is various form of psoriasis, but the most common form is plaque psoriasis [4]. The root cause of this skin disease is still unknown. However, the genetic fault is majorly evidenced as the cause of psoriasis [5]. Besides affecting the skin, it has an adverse impact on the quality of life because of its uncomfortable social presence and causes the risk of depression, stress, suicide, anxiety, etc. [6]. It is an incurable disease but can be controlled by regular and attentive treatments. Therefore, it's considered a major concern to healthcare organizations and society [7, 8].

Psoriasis Area Severity Index (*PASI*) is used most often and accepted as a gold standard by dermatologists to measure the amount of existence and severity of plaque-type psoriasis in the patient [9]. It leads to an easy score for monitoring this disease and is standardized in daily practice [10]. It combines both psoriasis area and severity scores from all the body regions of a psoriasis patient. The percentage area of the body affected with psoriasis is scored from 0 to 6 as shown in Table 1. While, each clinical severity present in psoriasis (i.e. redness, scaliness, and thickness) is stratified on a scale of 0 to 4 score. The stratification details of these clinical severity parameters are given in Table 2 [1, 9].

All four major human body regions i.e., head and neck part (*h*), upper extremities part (*ue*), trunk part (*t*), and lower extremities part (*le*) from both front and rear sides are examined for overall *PASI* measurement in a psoriasis patient. Different weights (W_i) are assigned to consider body parts based on the area covered on the body surface. Hence, the weights $W_h = 0.1$, $W_{ue} = 0.2$, $W_t = 0.3$, and $W_{le} = 0.4$ are included while measuring the overall *PASI* for a psoriasis patient (*PASI*_{patient}) that is represented by Eq. (1) [1, 9]. The maximum value of *PASI* for anybody region ($i \in \{h, ue, t, le\}$) is found to be equal to 72. Due to the consideration of the body part's weights, the value of overall *PASI* is nearly continuous and ranges from 0 to 72.

$$Overall \ PASI_{patient} = \sum_{i} W_i \times PASI_i = \sum_{i} W_i \times \left(\left(R_i + S_i + T_i \right) \times A_i \right)$$
(1)

In current practice, Dermatologists follow the visual inspection and the sense of touch to diagnose and further understand the existence and severity of this disease. This subjective approach required a highly skilled and experienced dermatologist. Also, manual assessment is usually a slow, hectic, and unreliable job for dermatologists. It also suffers from inter and intra-observer variability [11] and hence, fails to reproduce similar assessment reports. With so many subjective limitations, the psoriasis diagnosis, as well as monitoring, is a very tedious and challenging task [4, 12]. These subjective flaws can only be eliminated by adopting an objective approach [1]. Hence, the need

Psoriatic Lesion Area, Ar (in %)	0	< 10	10<30	30<50	50 < 70	70<90	90–100
Area Score (A)	0	1	2	3	4	5	6

 Table 1 PASI area scoring system [1, 9]

Table 2 Stratification	n details of each cl	linical severity present in psoriasis	(1, 9)	6	
	(Absent)	I (Mild)	2 (Moderate)	c (Severe)	4 (Very Severe)
Redness (R)	No redness	Light Red	Red, but not dark red	Dark red	Very dark red
Scaliness (S)	No scaling	Fine scaling covering some part of the lesion	Fine to rough scaling covering a large part of the lesion	Rough, thick scaling covering a large part of the lesion	Very rough, very thick scaling cover- ing the lesion
Thickness (T)	No elevation	Slight but definite elevation	Moderate elevation with rough edges	Marked elevation with sharp edges	Very marked elevation with hard edges

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for an objective assessment of psoriasis through a computer-aided diagnosis (CADx) system is clinically valuable and vital for dermatologists [13–16]. Dermatologists will benefit greatly from the CADx system for psoriasis since it will assist them with focused and reproducible diagnosis rapidly. This can also provide a good scope for researchers and medical experts to generalize behaviour or case studies, test hypotheses or theories, and discover new treatments as well [1, 17].

In this regard, many researchers have shown their interest and major contributions from objective segmentation of psoriasis lesions to its type and severity assessment from 2D digital images. To the best of our knowledge, a benchmark dataset of psoriasis is not available publicly to date. Therefore, every single research work on psoriasis uses a self-generated and private psoriasis image dataset [18, 19]. The objective approaches for the assessment of psoriasis lesions based on R, S, and T severity assessment are tabulated in Table 3. From Table 3, it can be observed that most of the existing research works are based on conventional image processing and/or machine learning (ML) algorithms [19]. In the ML paradigm, a manual feature engineering process is essentially required along with conventional image pre-processing steps. The manual extraction of relevant features is not an easy task and needs an expert from the domain of the dataset. This manual interaction makes ML approaches semi-automated and hence unreliable. The colour and texture features are used for redness and scaliness severity respectively in most of the ML approaches listed in Table 3 [20–24]. While not a single ML-based approach is developed for thickness severity scoring from 2D skin images. It can also be observed from Table 3 that these methods [20-24] are validated with less number of images.

Recent advancement of deep learning (DL) in computer vision and medical imaging domains has led to substantial improvement in performance and reliability over traditional ML techniques [19, 25, 26]. DL models extract different levels of reliable features automatically from digital images [27]. However, there is a limited amount of research work done based on a DL approach for psoriasis diagnosis [19]. In [28, 29], the DL

Author (Year)	#Images	Method (Features)	R	S	Т
Lu et al. [20] (2012)	88	KNN, SVM, DT (manual: colour, texture)	ACC: 0.79	ACC: 0.89	-
Banu et al. [21] (2014)	17	NN, NB, SVM (manual: colour, texture)	ACC: 0.92	-	-
Raina et al. [22] (2016)	80	LDA (manual: colour)	ACC: 0.49 ICC: 0.42	-	-
George et al. [23] (2018)	676	Patch-based dictionary learn- ing, RF, SVM	F1: 0.71	-	-
George et al. [24] (2019)	96	BoVWs, SVM, RF	-	ACC: 0.81	-
Pal et al. [28] (2016)	707	DCNN (automated)	ACC: 0.61	ACC: 0.59	ACC: 0.61
Pal et al. [29] (2018)	707	ResNet-50, MobileNet (auto- mated)	ACC: 0.61 MAE: 0.44	ACC: 0.63 MAE: 0.43	ACC: 0.64 MAE: 0.39

Table 3 Existing works on objective severity assessment of psoriasis lesions from cropped skin images

Accuracy (ACC); Bag-of-Visual-Words (BoVWs), Decision Tree (DT), Deep Convolutional Neural Network (DCNN), F1-score (F1), Intraclass Correlation Coefficient (ICC), K-Nearest Neighbour (KNN), Linear Discriminant Analysis (LDA), Mean Absolute Error (MAE), Naïve Bayes (NB), Neural Network (NN), Number of (#), Random Forest (RF), ResNet (Residual Network), Support Vector Machine (SVM) model is adopted for objective assessment of psoriasis lesions based on R, S, and T severities (refer to Table 3). These approaches [28, 29] are validated using a required large number of cropped skin images of psoriasis lesions compared to other approaches [20–24] listed in Table 3.

PASI area scoring of lesions is done with reference to the healthy skin of the respective body region. Hence, PASI can't be evaluated objectively only from cropped psoriasis lesions [1, 9, 16]. For this, the objective approach should be applied to images of different body regions for psoriasis patients. Only a few research works [30-36] have estimated A, R, S, T, and PASI from full-body 2D digital images of psoriasis patients using the ML or DL framework in the recent past. In [30], a two-stage ML algorithm is designed for measuring the psoriasis area where k-means clustering is implemented for segmentation on the images of two distinct colour spaces in two stages. A singlestage DL framework is designed in [31] for the automatic estimation of A using a modified UNet model. In [32], the conventional image processing algorithm is designed for objective scoring of each parameter of PASI and overall PASI too but validated on less number of test images. PSENet model based on DCNN with Siamese structure is proposed in [33]. This model directly estimates only PASI for a given input image without estimating any parameter of PASI. In [34], the PSENet model proposed in [33] is modified by introducing lesion attention modules (LAMs) for the measurement of PASI parameters which eventually gives the final PASI score for the image. In [35], a pretrained ResNet18 model is adopted and fine-tuned to measure R, S, and T severities on an entire image. Moreover, the most important parameter of PASI i.e. A, is also estimated by the same classification model without segmenting psoriasis lesions from the image. Additionally, images with an area score of 6 and a severity score of 4 are not considered.

In this paper, a deep learning-based fully automated system for objective evaluation of PASI from 2D digital images by automatic severity assessment of segmented psoriasis lesions. A lightweight backbone network (i.e., MobileNetV2 [36]) is adopted in the UNet segmentation model with a transfer learning paradigm in this work for automatically segmenting the psoriasis lesion from the healthy skin for objective estimation of psoriasis area score (i.e., A). Further, the severity assessment of the segmented psoriasis lesion based on R, S, and T scores is performed automatically by the proposed classification model. The proposed classification model is developed by amalgamating a lightweight CNN model (i.e., MobileNetV2 [36]) and Vision Transformer (ViT) [37, 38]. The pre-trained Mobile-NetV2 model is adopted as a backbone CNN for local processing while ViT operates as a simple convolution for global processing. With this fusion, both local and global representations are learned effectively and efficiently by the proposed model. The class weighting, transfer learning, and data augmentation approaches are also utilized in the proposed model to deal with data imbalance and insufficiency issues [39-45]. These fusions of networks and approaches result in a better model for the intended task. The main contributions of the proposed work can be summed up as follows:

- The proposed work is fully automated and designed for objective PASI scoring from 2D images along with the segmentation of healthy skin and psoriasis lesion regions.
- (ii) The experiments are conducted on the large self-prepared dataset with a considerable number of all *PASI* area and severity score images. It is validated with a five-fold cross-validation technique. The proposed classifier model is also found to be more potent and computationally efficient for the intended task when compared to other DL models.

- (iii) The result of each model is analyzed by computing various performance metrics with and without ± 1 tolerance. Intraclass Correlation Coefficient (ICC) is also computed which is an important statistical tool to measure the reliability of scoring.
- (iv) All the severity parameters of *PASI* are estimated by considering each plaque-psoriasis lesion in the digital body images of a psoriasis patient, which results in an adequate scoring for *PASI* when compared to other related works from the literature.

The remaining sections of the paper are organized as follows. Section 2 presents the methodology for objective scoring of *PASI*. Section 3 covers a detailed description of data and experimentations. The experimental results for each module of the proposed system with the evaluation of different performance metrics are demonstrated in Section 4. The ablation and comparative study analyses are done in Section 5. The research study is concluded in Section 6 and then, followed by recommendations for future research.

2 Methodology

The proposed system is designed to estimate the *PASI* objectively from a 2D digital image of a plaque-psoriasis patient by predicting the area score (A) and three severity parameters (R, S, and T) scores. For this, the proposed system includes a segmentation model for the area and three classification models for each clinical severity. The overall flow diagram of the proposed methodology is illustrated in Fig. 1. The input used for the proposed work is in the form of raw 2D colour photographic images. The first stage of the proposed system consists of a segmentation module. In the segmentation module, psoriasis lesions from the



Fig. 1 Proposed system for the objective calculation of PASI

skin region are automatically segmented. This automatically segmented image can be used for the objective estimation of A. Each segmented lesion from an input image of the first stage is fed as an input to the second stage. In the second stage, the severity scores based on R, S, and T factors are predicted automatically by the classification module. The classification module consists of three identical DL-based classification models for severity classification of R, S, and T. Lastly, the *PASI* for an input image is evaluated with the help of predicted scores of A, R, S, and T from the above methods.

2.1 Lesion segmentation module

In the first stage, a single-stage lesion segmentation module is used for the automatic calculation of the psoriasis lesion area percentage. The segmentation module is based on the architecture of a UNet model [46] having a lightweight MobileNetV2 network as a backbone. This model will perform multi-class segmentation of the image that will classify each pixel of the image into three different labels namely background, healthy skin, and psoriasis lesions simultaneously. The input of this segmentation model is a 2D RGB digital image of size 512×512 that results in an input shape of $512 \times 512 \times 3$. Due to the symmetry nature of UNet, the output size is the same as the input size (i.e., 512×512). Therefore, the shape of the segmented output mask becomes $512 \times 512 \times 3$ due to the multi-segmentation of three regions (i.e., background, healthy skin, and psoriasis lesion).

This module has two paths i.e. encoder and decoder that are connected U-shape. The encoder part of the model has a pre-trained MobileNetV2 network [36] for high-dimensional and relevant feature extraction which is further finely trained with the psoriasis dataset. MobileNetV2 network utilizes a linear bottleneck and inverted residual having depth-wise separable and pointwise convolution layers along with a residual connection. The use of depthwise separable convolution is not computationally expensive compared to standard convolution and hence makes the network lightweight. This versatile nature of the MobileNetV2 network allows easy training and makes it a popular backbone as a better and faster local feature extractor for several computer vision tasks [36]. The inner layer of this network exhibits the ability to switch the lower-level concepts like pixels to higher-level descriptors like image categories, while the bottlenecks encapsulate the network's intermediary inputs and outputs. The short identity connection between the input and output of the block resembles a standard residual connection for improved performance. This backbone network comprises a sequence of convolution and bottleneck operations in five stages. In each stage, the receptive field of input is continuously increased whenever the input size is reduced by half. The details of layers in each stage with bottleneck and inverted residual design are stated in [36]. It performs local processing and extracts relevant and deep local feature representative maps of high spatial dimension. The decoder path expands the encoded features stage-wise to get the final segmented output of the same size as the input. The layer-wise details of the decoder path can be found in [31].

The percentage of skin area (i.e., Region of Interest, ROI) covered by psoriasis can be calculated with the help of Eq. (2). For this segmentation task, the total number of pixels belonging to psoriasis lesion region (N_P) in the segmented mask output corresponds to the area of psoriasis lesion. The representation for skin region i.e., ROI area in the segmented mask output is the total number of pixels predicted as healthy skin (N_H) or psoriasis lesion (N_P) . Therefore, Eq. (2) can be modified into Eq. (3) for the calculation of the percentage of psoriasis area (Ar) over the skin with the help of an automatically segmented mask.

Based on the calculated percentage value of the psoriasis lesion area, the area score (A) parameter for *PASI* can be obtained using Table 1.

$$Psoriasis Area, Ar(in\%) = \frac{Area \ of \ psoriasis \ lesion}{Area \ of \ ROI} \times 100\%$$
(2)

$$Psoriasis Area, Ar(in\%) = \frac{N_P}{N_H + N_P} \times 100\%$$
(3)

The automatically segmented psoriasis lesion image is obtained by overlaying the input RGB image with the segmented mask output. The area percentage of each psoriasis lesion (Ar_l) in the segmented mask output is also measured using Eq. (4) as shown below:

$$Ar_{l}(in\%) = \frac{N_{P_{l}}}{N_{H} + N_{P}} \times 100\%$$
(4)

where; N_{P_l} be the number of pixels belonging to each psoriasis lesion (*l*) and the sum of Ar_l of all the individual segmented lesions in an image became equal to Ar. Further, the segmented lesions are cropped as per the closest bounding box to be fed as input to the second stage of the proposed work.

2.2 Lesion severity classification module

In the second stage, the objective assessment of the severity scores of lesions is done using a classification module. In this module, three identical DL-based classification model is designed and trained for each of the clinical severity parameters of *PASI (R, S,* and *T*). The model proposed for the severity classification task is developed and designed by combining lightweight CNN and ViT networks in series. In CNN, the properties of spatial inductive biases allow the network to learn local representations even with fewer parameters for different computer vision tasks [47]. One of the most popular lightweight networks that perform well for image classification tasks is MobileNetV2 [36]. Therefore, MobileNetV2 is selected as a lightweight backbone CNN to perform automatic local feature processing from the target dataset. ViT is based on multiple self-attention networks and shows a great performance for visual-related tasks due to input-adaptive weighting and global information learning [48]. ViT network in the proposed model operates as a standard convolution and thus, has convolution-like properties [38]. The proposed model incorporates properties of both CNN and ViT in the interest of building a high-performing and lightweight hybrid model for the intended task.

The architecture of the proposed model is represented in Table 4. The input RGB image of shape $128 \times 128 \times 3$ is fed as input to the model. The input image is passed through a MobileNetV2 [36], which is pre-trained on the *ImageNet* dataset [49] (i.e., source) and fine-tuned with the psoriasis lesion dataset (i.e., target) for the intended task. The output shape of the local feature representative map generated automatically by the MobileNetV2 backbone network from the input image of $128 \times 128 \times 3$ shape is $4 \times 4 \times 1280$.

The high-dimensional local feature representative is projected to a point-wise convolution (having 64 filters) to capture and learn the linear combinations of input channels. Then, the convolved feature map is processed by ViT to capture long-range dependencies that represent global features [38, 50]. The structure of ViT to act as a simple convolution operation in the proposed model is illustrated in Fig. 2. ViT is used as a typical convolution

lable 4 Architecture of the proposed c	lassincation model (Mot	DIENELV 2 + VII)		
Layer		Details	Output shape	Connected to
Input (2D image)		RGB	(128,128,3)	ı
MobileNetV2		Backbone	(4,4,1280)	Input
Conv2D_#1		Filter: (1×1) , 64	(4,4,64)	MobileNetV2
Reshape_#1		Unfolding into patch of 2×2	(4,4,64)	Conv2D_#1
LN_#1		Layer Normalization	(4,4,64)	Reshape_#1
МНА		Multi-Head Attention (No. of head: 2, Projec- tion dimension: 64)	(4,4,64)	LN_#1, LN_#1
Add_#1		Skip Connection	(4,4,64)	MHA, Reshape_#1
LN_#2		Layer Normalization	(4,4,64)	Add_#1
MLP	Dense_#1	Units: 128	(4,4,128)	LN_#2
	Dense_#2	Units: 64	(4,4,64)	Dense_#1
Add_#2		Skip connection	(4,4,64)	Dense_#2, Add_#1
Reshape_#2		Folding into conv-like feature maps	(4,4,64)	Add_#2
Concatenate		Local & Global feature-maps	(4,4,128)	Conv2D_#1, Reshape_#2
Conv2D_#2		Filter: (1×1) , 64	(4,4,64)	Concatenate
GAP2D		Global Average Pool 2D	(64)	Conv2D_#2
Output (Dense_#3 + Softmax)		Units: 5	(5)	GAP2D
2D Convolution (Conv2D), 2D Global .	Average Pooling (GAP2	D), Layer Normalization (LN), Multi-Head Attention (MHA), Multi-Layer Per	ceptron (MLP)



Fig. 2 Structure of ViT for operating as convolution

involving unfolding, deeper global processing (replaces local processing in convolutions), and folding operations. The convolved feature map of resolution (H, W, k) is unfolded into small patches of considered sizes (i.e., 2×2) in a series. This results in *N* number of non-overlapping small patches of feature map having a resolution of (P, N, k) where *P* represents the area of small patch and $N = (H \times W)/P$.

After being unfolded, this flattened vector of patches is then passed through a transformer block. This block is based on several self-attention layers that replicate long-range dependencies. It encodes the inter-patch relationships by interacting with each other to learn global representation. The global learning from the convolved feature map leads to better global representation [50]. The transformer block is generally made up of three significant processing components: Layer Normalization (LN), Multi-Headed Attention (MHA), and Multi-Layer Perceptron (MLP) [37]. LN controls the training process and enables the model to adjust to the differences between the training images. With MLP, attention maps are generated to keep the focus on important regions in the image. The input feature maps of the transformer block are added with concatenated attention maps before feeding forward to the MLP. MLP is used as an output of the transformer consisting of two fully connected layers to generate the encoded representations [37]. The final encoded global representation of the transformer block is obtained by adding the concatenated attention map output of MHA and the encoded representation output of MLP (refer to Fig. 2).

The local processing step of the convolution operation is replaced with deeper global processing in VIT. With this, the spatial information and patch order of pixels within each patch are not lost as happens in the case of standard ViT [37] and thus, the positional encoding operational layer of standard ViT is not required. The output of the transformer block is folded back again into a resolution of (H, W, k) to resemble a feature representation produced by a convolution operation. Thus, ViT operates more like a convolution despite a transformer and outputs a feature map having a respective field similar to the input feature map (i.e., $H \times W$). This offers a different perspective to encode global representation that exhibits convolution-like properties such as spatial inductive biases, easy-to-learn/train/ optimize, faster computation, etc. [38].

After the folding operation, the resolution of local and global feature representation maps became similar and both of these features are concatenated. The concatenated feature map is further fused by passing through a point-wise convolutional layer having filters equal to the channel size of the local or global feature i.e., 64 in this work. With this, the fused feature map efficiently encrypts both local and global representation with unchanged resolution. The fused feature map representation passes through a 2D global average pooling layer (GAP2D). GAP2D applies the average to H and W of the input feature map for all channels (k) [51, 52]. Lastly, a dense layer having the number of nodes equal to the total classes and

softmax activation function is used in the output. The *softmax* helps in producing the final output of the model in terms of class probabilities within the range of [0,1] for each class.

2.3 Objective calculation of PASI

After the automated severity assessment of each segmented psoriasis lesion (*l*), the final severity scores (i.e., R_f , S_f , and T_f) of an input image are calculated based on the estimated area contribution and severity scores of each lesion present in the corresponding image. The mathematical equation for obtaining the final severity scores is represented by Eq. (5) which calculates the mean. The consideration of severity scores of each lesion based on its area leads to the effective calculation of the final severity score as well as *PASI* for an input image. In this way, all the parameters of *PASI* are estimated objectively and the objective calculation of PASI for an input image (*PASI_{im}*) can be done using Eq. (6). With the proposed work, it is also possible to calculate the overall *PASI* for a psoriasis patient using Eq. (1). For overall *PASI*, *PASI_{im}* should be calculated for both front and rear images of all four body regions of a psoriasis patient by the proposed system.

$$R_{f} = \frac{\sum_{l} (R_{l} \times Ar_{l})}{\sum_{l} Ar_{l}}; S_{f} = \frac{\sum_{l} (S_{l} \times Ar_{l})}{\sum_{l} Ar_{l}}; T_{f} = \frac{\sum_{l} (T_{l} \times Ar_{l})}{\sum_{l} Ar_{l}}; where Ar = \sum_{l} Ar_{l}$$
(5)

$$PASI_{im} = \left(R_f + S_f + T_f\right) \times A \tag{6}$$

3 Data and experimentation details

3.1 Dataset details

For various skin diseases having lesions, dermatoscopy is used as a standardized image acquisition device [53, 54]. But for psoriasis, there is no such standardized image acquisition device or equipment exists. Hence, the psoriasis database is not available publicly anywhere. This left researchers with no option to self-prepare private psoriasis image databases using 2D digital cameras for psoriasis research [1, 16, 19].

In this work, the plaque-type psoriasis database was collected from the Psoriasis Clinic and Research Centre, Psoriatreat, Pune, Maharashtra, India. The digital images are obtained under the supervision of a team of dermatologists from Indian psoriasis patients irrespective of age, gender, and community. The database was generated with ethical approval and was anonymized. The digital images are acquired in an uncontrolled environment with an automatic setting using a Sony NEX-5 digital camera with a 22 mm lens and 350 dpi. The images are processed with an RGB colour depth of 24 bits per pixel in the Joint Photographic Expert Group (JPEG) format. All the major body regions of the patients i.e., upper extremities, trunk, and lower extremities from both front and rear sides are considered while capturing data. The sample images from the considered body region of psoriasis patients are shown in Fig. 3. However, head region images are not taken into account due to the patient's privacy. For segmentation, the ground truth mask is labelled by the team of dermatologists for each image. Further, the severity of each psoriasis lesion is categorized into five different classes (i.e., none, mild, moderate, severe, and very severe). These annotations are also prepared with the help and support of a team of dermatologists



Fig.3 Sample images from different body regions of psoriasis patients. (a) Trunk (b) Upper extremities (c) Lower extremities

based on all three severity parameters of PASI (i.e., R, S, and T). Figure 4 shows the sample skin images of psoriasis lesions under different severity scores of redness, scaliness, and thickness.

The self-prepared psoriasis image dataset contains 1,018 images of considered body regions from 212 psoriasis patients having a total of 5,075 psoriasis lesions. The distribution of lesions in each severity class of *R*, *S*, and *T* are tabulated in Table 5 which shows imbalanced data. Initially, 50 out of 212 patients were randomly selected as the test dataset for the proposed work that contains 350 images and 1,420 lesions. For the proposed severity classifier model, the remaining 162 patients that has 3,655 lesions from 668 images are considered for training and validation purpose using a stratified five-fold cross-validation technique [55]. With a five-fold stratified split, the ratio of training and validation data sets is 4:1. The simple pre-processing is done by resizing images of body regions into a common size of 512×512 for the segmentation task. The automatically segmented skin patch images of plaque psoriasis lesions are resized into a common size of 128×128 for the classification task.

3.2 System implementation details

All the models have been built using Python programming language [56] with the Keras API [57] and TensorFlow backend engine [58]. The experiment was conducted on a workstation having an Intel Xeon Silver CPU with 64GB RAM and NVIDIA Quadro P4000 GPU with 8GB memory. For efficient computation, pixel values of all the images are normalized into the range of [0,1]. The data augmentation and class weighting approaches are utilized to deal with data inadequacy and imbalance. The automatic data augmentation technique



Fig. 4 Sample images of psoriasis lesions in each severity class. (a) Redness (b) Scaliness (c) Thickness

Class Label	Redness (R)	Scaliness (S)	Thickness (T)
0	240	552	348
1	724	1,654	1,663
2	1,874	1,127	1,322
3	642	256	211
4	175	66	111
Total	3,655	3,655	3,655

is applied randomly to generate augmented images during the training of the model using the Keras library [57]. The balanced class weight values [59] for our imbalanced psoriasis dataset are computed and assigned during model training. For further training/testing of the proposed severity classification module, the hyperparameter details are tabulated in Table 6. The hyperparameter details of the segmentation model are the same as described in [31].

4 Result

Table 5Number of psoriasislesions in each severity class

The performance is evaluated for each module of the proposed system and is presented in this section. For the segmentation module, the two potent segmentation performance metrics namely Dice-Coefficient Index (DI) and Jaccard Index (JI) are evaluated [62]. Due to the imbalanced number of lesions in different severity classes (refer to Table 5), the weighted averaging method is used for evaluating multi-class classification metrics (i.e.,

Hyperparameter	Details
Train & test percentage ratio	5-fold cross-validation (80:20) [55]
Batch Size	32
Epochs	150
Loss Function	Categorical cross-entropy loss [60]
Optimizer function (learning rate)	ADAM [61] (adaptive; starting with 0.001)
Online Data Augmentation (during training only)	Image rotation, shifting, flipping, zooming, and shearing

Table 6 Hyperparameter details for the model implementation

Precision, Recall, and F1-score) for the severity classification module [63, 64]. The multiclass Receiver Operating Characteristic (ROC) curve [65] analysis is also performed along with the computation of the area under the ROC curve (AUC) [66] for each severity class. In addition, the overall Accuracy (ACC) [63], Mean Absolute Error (MAE) [67, 68], and Intraclass Correlation Coefficient (ICC) [69] are also computed for evaluating the performance of the proposed system for automatic scoring of each parameter of *PASI* and *PASI* for a 2D RGB image of a psoriasis patient. ACC value close to 1 while an MAE value close to 0 indicates a better model's performance [35]. ICC values lie in the range of [0,1]; where values lower than 0.5, between 0.5 and 0.75, between 0.75 and 0.9, and upper than 0.9 resembles the poor, moderate, good (acceptable), and high (adequate) level of agreement respectively [35, 69]. ACC and MAE metrics are also evaluated by considering the maximum variation of score 1 between automated and annotated scores (i.e., with ± 1 score tolerance) for each parameter of *PASI* [28, 29]. This is done in favour of concerning inter- and intra-observer variability issues from which psoriasis severity scoring suffers [1, 4, 11].

4.1 Result for segmentation module

The region-wise and overall segmentation result achieved by the segmentation model is tabulated in Table 7. The metrics value for the psoriasis lesion region is found to be less compared to the other two regions of healthy skin and background. This is due to the lower percentage distribution and high irregularity in the shape, size, number, dispersion, severity, noise, boundaries, etc. properties of the different lesions compared to the other two regions. However, the overall metrics result achieves values greater than 0.90 which represents good segmentation performance. Therefore, the automatic segmentation of psoriasis lesions by segmentation module is used for objective estimation of psoriasis area score (A). The final results achieved for the objective estimation of A using ACC, MAE, and ICC metrics are

Table 7Performance forpsoriasis lesion segmentation	Region	Segmentation pe metrics	Segmentation performance metrics		
		DI	JI		
	Background	0.9822	0.9651		
	Healthy Skin	0.9769	0.9548		
	Psoriasis Lesion	0.9334	0.8750		
	Overall	0.9641	0.9316		

0.9548, 0.0452, and 0.9490 respectively. With ± 1 score tolerance, ACC and MAE become 1.00 and 0.00 respectively as the value of absolute error observed is either 0 or 1 only. The visual segmentation results for sample two input images are presented in Fig. 5. These overall results confirm the better potential of the proposed segmentation model for the intended task.

4.2 Result for classification module

In this sub-section, the classification result is evaluated based on the severity prediction of each psoriasis lesion that is segmented automatically by the segmentation module of the proposed system. The performance of the proposed classifier model is acquired with 5-fold cross-validation for better generalizability. The average and fold-wise results of different performance metrics are tabulated in Tables 8, 9, and 10 for R, S, and T severities respectively. The average F1-score and overall ACC are greater than 0.75 and MAE is less than 0.30 for all three severity parameters in each fold. Also, the standard deviation among the folds is lower than 0.03. This shows the satisfactory and consistent performance of the proposed model in each fold for all severity parameters of PASI. The fold-average ACCs achieved for R, S, and T severities are 0.7903, 0.7764, and 0.8043 respectively. In addition, the values of the average F1-score and overall ACC are equal up to two decimals in each fold. Despite an imbalanced dataset, the proposed model is able to achieve stable performance for complex multiclassification without getting highly biased towards the majority class. Also, the ICC value is found to lie in the range of 0.75–0.90 in each case signifying overall good agreement between automated and manual severity scoring. The average value of ICC for R, S, and T severities achieved are 0.7997, 0.8084, and 0.8342 respectively. The severity results with ± 1 score tolerance for each case are tabulated in Table 11. From Table 11, it can be observed that the fold-average value of ACC became greater than 0.95 and MAE became less than 0.08 when



Fig. 5 Visual segmentation result (a) Input image, (b) Ground truth mask (gt), (c) Predicted mask (pred), and (d) Performance metrics

Performance metrics (for Rscore)		f0	f1	f2	f3	f4	folds avg.	Folds std. (±)
Weighted averaging	Precision	0.7985	0.7841	0.8189	0.7588	0.8328	0.7986	0.0260
	Recall	0.7971	0.7705	0.8049	0.7515	0.8275	0.7903	0.0266
	F1	0.7919	0.7688	0.8046	0.7512	0.8252	0.7895	0.0263
	AUC	0.9581	0.9522	0.9574	0.9490	0.9633	0.9560	0.0050
Overall ACC		0.7971	0.7705	0.8049	0.7515	0.8275	0.7903	0.0298
MAE		0.2480	0.2705	0.2361	0.2854	0.2094	0.2499	0.0265
ICC		0.7868	0.7874	0.8004	0.7943	0.8297	0.7997	0.0158

Table 8 Performance for redness severity scoring using the proposed classification model

Table 9 Performance for scaliness severity scoring using the proposed classification model

Performance metrics (for S score)		f0	f1	f2	f3	f4	folds avg.	Folds std. (±)
Weighted averaging	Precision	0.7652	0.8073	0.7623	0.7901	0.7683	0.7786	0.0174
	Recall	0.7664	0.8053	0.7577	0.7844	0.7680	0.7764	0.0168
	F1	0.7625	0.8002	0.7542	0.7781	0.7666	0.7723	0.0159
	AUC	0.9438	0.9577	0.9414	0.9470	0.9536	0.9487	0.0061
Overall ACC		0.7664	0.8053	0.7578	0.7844	0.7680	0.7764	0.0168
MAE		0.2439	0.2070	0.2710	0.2320	0.2485	0.2405	0.0210
ICC		0.8178	0.8347	0.7714	0.8106	0.8075	0.8084	0.0208

Table 10 Performance for thickness severity scoring using the proposed classification model

Performance metrics (for T score)		f0	f1	f2	f3	f4	folds avg.	Folds std. (±)
Weighted averaging	Precision	0.8330	0.8116	0.7704	0.8265	0.7989	0.8081	0.0223
	Recall	0.8238	0.8156	0.7639	0.8234	0.7947	0.8043	0.0228
	F1	0.8213	0.8113	0.7617	0.8242	0.7906	0.8018	0.0233
	AUC	0.9559	0.9589	0.9650	0.9661	0.9702	0.9632	0.0051
Overall ACC		0.8238	0.8156	0.7639	0.8234	0.7947	0.8043	0.0228
MAE		0.1783	0.2070	0.2567	0.1992	0.2177	0.2118	0.0259
ICC		0.8749	0.8220	0.8021	0.8351	0.8370	0.8342	0.0239

 ± 1 score tolerance is allowed. Hence, ACC and MAE values for *R*, *S*, and *T* severities are found to be significantly improved with ± 1 score tolerance.

The class-wise performance over all possible thresholds is summarized by plotting the ROC curve [65] and calculating AUC [66]. The ROC curves for the best fold of each severity are illustrated in Fig. 6. From Tables 8, 9, and 10, it can be observed that the folds f4, f1, and f0 for R, S, and T achieve the best classification performance respectively compared to other folds. Hence, Fig. 6a, b, and c represents the ROC curves of best fold f4 for R, f1 for S, and f0 for T respectively. From the ROC curves of Fig. 6, it can be observed that the average AUC score in each class of R, S, and T

13	14	folds avg.	folds std. (±)
10 0.9630	0.9630	0.9614	0.0023
0.0739	0.0739	0.0788	0.0052
53 0.9836	0.9856	0.9848	0.0053
0.0329	0.0308	0.0320	0.0116
0.9795	0.9877	0.9852	0.0071
0.0431	0.0246	0.0308	0.0150
	13 10 0.9630 01 0.0739 53 0.9836 33 0.0329 15 0.9795 90 0.0431	13 14 10 0.9630 0.9630 01 0.0739 0.0739 53 0.9836 0.9856 33 0.0329 0.0308 15 0.9795 0.9877 90 0.0431 0.0246	f3 f4 folds avg. 10 0.9630 0.9630 0.9614 01 0.0739 0.0739 0.0788 53 0.9836 0.9856 0.9848 33 0.0329 0.0308 0.0320 15 0.9795 0.9877 0.9852 90 0.0431 0.0246 0.0308

Table 11 Performance for automated severity scoring using the proposed classification model with ± 1 score tolerance

severity is greater than or equal to 0.9. This indicates the desirable performance of the proposed model in discriminating between the actual and other classes.

4.3 Result for objective estimation of PASI

The result presented in this sub-section is evaluated considering images of psoriasis patients from test datasets. Table 12 represents the performance for automatic estimation of each parameter of PASI and objective measurement of the final PASI for an image of a psoriasis patient. From Table 12, it can be observed that ACC achieved for automatic estimation of R, S, T, and A are 0.7971, 0.7943, 0.8000, and 0.9600 respectively. For *PASI*, the ACC can't be considered an ideal performance metric because it is not possible to correctly predict the PASI whose numeric values are nearly continuous that ranges from 0 to 72. Therefore, the MAE metric is computed for PASI and achieved a value of 1.0200. The MAE values of 0.2314, 0.2200, 0.2086, and 0.0400 are achieved for R, S, T, and A respectively. With ± 1 score tolerance limit, a significant amount of improvement can be observed from Table 12 in the automatic scoring of each parameter of *PASI*. After considering ± 1 error, the value of ACC becomes [R:0.9714, S:0.9857, T:0.9914, A:1.0000] and MAE becomes [R:0.0571, S:0.0285, T:0.0171, A:0.0000]. For PASI, the value of MAE decreases from 1.0200 to 0.8029 with ± 1 score tolerance. The ICC values achieved for R, S, and T parameters are 0.7806, 0.8024, and 0.8205 which lie between the range of 0.75-0.9 indicating good agreement. The ICC value of 0.9630 (i.e., greater than 0.9) achieved for the most important parameter of PASI i.e., A indicates a high level of agreement. Therefore, the objective calculation of the *PASI* score from the proposed system also achieves an adequate agreement level with an ICC value of 0.9100. These results overall signify that the proposed system has significant potential for the objective evaluation of *PASI*.

5 Discussion

5.1 Ablation study on the proposed classification model

The effect of ViT in the proposed model is validated by removing it from the model. Without ViT, the model is left with only the MobileNetV2 network as the backbone CNN for local





(c) Thickness, T (f0)

Performance metrics	Tolerance limit	R	S	Т	A	PASI
ACC	without	0.7971	0.7943	0.8000	0.9600	_
	with ± 1	0.9714	0.9857	0.9914	1.0000	-
MAE	without	0.2314	0.2200	0.2086	0.0400	1.0200
	with ± 1	0.0571	0.0285	0.0171	0.0000	0.8029
ICC		0.7806	0.8024	0.8205	0.9630	0.9100

 Table 12
 Performance for objective PASI scoring using the proposed system

Table 13 Performance comparison of proposed model with and without (w/o) ViT for lesion severity classification

Metrics	R		S		Т	
	w/o ViT	with ViT	w/o ViT	with ViT	w/o ViT	with ViT
Precision	0.7665	0.7985	0.7379	0.7652	0.8039	0.8330
Recall	0.7602	0.7971	0.7377	0.7664	0.7992	0.8238
F1	0.7537	0.7919	0.7349	0.7625	0.7992	0.8213
AUC	0.9563	0.9581	0.9438	0.9524	0.9559	0.9641
ACC	0.7602	0.7971	0.7377	0.7664	0.7992	0.8238
MAE	0.2541	0.2480	0.2725	0.2439	0.2131	0.1783
ICC	0.7522	0.7868	0.7970	0.8178	0.8488	0.8749

 $\label{eq:table_$

Metrics	R		S		Т	
	w/o class-weight	with class-weight	w/o class-weight	with class-weight	w/o class-weight	with class-weight
Precision	0.7701	0.7985	0.7470	0.7652	0.7778	0.8330
Recall	0.7787	0.7971	0.7480	0.7664	0.7766	0.8238
F1	0.7697	0.7919	0.7427	0.7625	0.7692	0.8213
AUC	0.9464	0.9581	0.9487	0.9524	0.9573	0.9641
ACC	0.7787	0.7971	0.7480	0.7664	0.7766	0.8238
MAE	0.3074	0.2480	0.2664	0.2439	0.2398	0.1783
ICC	0.6853	0.7868	0.7868	0.8178	0.8488	0.8749

processing and decision-making layers having a GAP2D and a fully connected layer with a *softmax* activation function. For this, the implementation and experimentation of the model without and with ViT are performed on a similar computing platform and with the same train/ test dataset (i.e., from fold f0). The comparison of performance achieved by both of these models is made in Table 13. From Table 13, the gain in the value of each performance metric with ViT can be observed for all three severity parameters of *PASI*. This validates that the integration of ViT in the model augments the classification performance for the intended task.

Normalized confusion matrix





5.2 Impact of class weighting

The performance comparison of the proposed model with and without class weight for the lesion severity classification task with the same train/test dataset (i.e., from fold f0) is made in Table 14. From Table 14, it can be observed that there is a boost in the classification performance of the proposed model with class weighting. Due to class imbalance in

Normalized confusion matrix

DL models	R		S		Т		Trainable
	F1	ACC	F1	ACC	F1	ACC	(in Million)
DCNN [28]	0.6137	0.6316	0.5873	0.6172	0.6313	0.6391	24.0
CNN+XGBoost [71]	0.6285	0.6481	0.6043	0.6301	0.6491	0.6571	0.4
Modified VGG [16]	0.6594	0.6637	0.6016	0.6301	0.6763	0.6821	8.9
ResNet18 [35]	0.7395	0.7481	0.7212	0.7277	0.7784	0.7838	10.8
ResNet50 [29]	0.7194	0.7285	0.7095	0.7217	0.7591	0.7707	23.6
MobileNet [29]	0.7408	0.7511	0.7278	0.7289	0.7908	0.7973	3.2
Proposed model (MobileNetV2+ViT)	0.7919	0.7971	0.7625	0.7664	0.8213	0.8238	2.4

Table 15 Comparison between different DL models for psoriasis severity assessment on the same d

the dataset, the normalized confusion matrix [70] is also plotted for better insights into the impact of class weighting in the multi-classification task. The normalized confusion matrix of the proposed model with and without class weight are illustrated in Fig. 7. The confusion matrix without class weight (refer to Fig. 7a, c, and e) shows the higher diagonal value (i.e. correct prediction rate) and lower off-diagonal value (i.e. misclassification/error rate) only for the classes having a higher number of observations. From Fig. 7b, d, and f, it can be observed that the diagonal values are very high compared to off-diagonal values in each class of the normalized confusion matrix of the model trained with class weight. This validates that the class-weighting addresses the class imbalance in the model and thus, leads to a good classification model despite imbalanced data.

5.3 Comparative study for psoriasis severity assessment

The proposed model for severity assessment of psoriasis lesions is compared with other existing DL models from the literature [16, 28, 29, 35, 71]. This comparison is made based on both multi-class classification performance and the number of trainable parameters in the model. Table 15 tabulates the comparison of the proposed model with different DL models implemented for the intended task. The implementation and experimentation of these models are performed on a similar computing platform and with the same train/test dataset (i.e., from fold f0). The class weight and data augmentation are adopted with all the models while training. The transfer learning concept is involved with standard CNN models (i.e., ResNet18 [35], ResNet50 [29], MobileNet [29]) by using pre-trained weights trained on *ImageNet* and fine-tuning them with our psoriasis lesion dataset. From Table 15, it can be observed that the performance of the proposed model is comparatively higher compared to that of other DL models. Also, the proposed model provides a good balance between performance and trainable parameters.

5.4 Comparative study for objective PASI scoring

The proposed work is compared with other existing recent works [30–35] for objective scoring of *PASI* or any one of the *PASI* parameters from 2D digital images of psoriasis patients in Table 16. From Table 16, it can be observed that only the proposed work utilizes both DL-based segmentation (i.e., MobileNetv2 + UNet) and classification (MobileNetv2 + ViT) models for automated scoring of lesion area (*A*) and severity (*R*, *S*, *T*), respectively. Also,

Author (Year)	#total images	Method	Result achieved for objec	tive scoring of P/	ASI and its parame	eters	
	(#test images)		A	R	s	Т	PASI
Fink et al. [32] (2018)	160 (160)	Image Processing	ICC: 0.84	ICC: 0.74	ICC: 0.78	ICC: 0.82	ICC: 0.83
Tancharoen et al. [30] (2019)	10 (10)	K-means Clustering	ACC: 0.90	×	×	×	×
Li et al. [33] (2020)	5,205 (1,041)	PSENet (DCNN with Siamese structure)	×	×	×	×	MAE: 2.21
Wu et al. [34] (2021)	5,205 (544)	PSENet + LAMs	ACC: 0.55 MAE:0.63	ACC: 0.60 MAE: 0.46	ACC: 0.54 MAE: 0.49	ACC: 0.50 MAE: 0.48	MAE: 3.12
Raj et al. [31] (2021)	350 (70)	Modified UNet	ACC: 0.89	×	×	×	×
Schaap et al. [35] (2022)	1,731 (327)	ResNet18	ACC: 0.79 MAE: 0.21 ICC: 0.83	ACC: 0.67 MAE: 0.35 ICC: 0.71	ACC: 0.63 MAE: 0.35 ICC: 0.59	ACC: 0.74 MAE: 0.27 ICC: 0.66	×
Proposed work	1,018 (350)	MobileNetV2+UNet, MobileNetV2+ViT	ACC: 0.96 MAE: 0.04 ICC: 0.96	ACC: 0.80 MAE: 0.23 ICC: 0.78	ACC: 0.79 MAE: 0.22 ICC: 0.80	ACC: 0.80 MAE: 0.21 ICC: 0.82	MAE: 1.02 ICC: 0.91

Table 16 Comparison of literature work with the proposed work for objective scoring of PASI parameters from 2D images of psoriasis patients

the proposed work is the only single and fully automated research work in Table 16 that provides objective scoring of *PASI* by finding all the parameters of *PASI* with simultaneous automated segmentation of psoriasis and healthy regions. However, the existing works [30, 31] performs segmentation task for objective scoring of the *A* parameter only. While the remaining existing works [33–35] only performs classification task for objective scoring without segmenting the psoriasis lesion. Due to both segmentation and classification tasks, the performance achieved by the proposed work for objective scoring of *PASI* is better compared to other existing works. The objective severity assessment of an image by considering all the severity levels from each segmented psoriasis lesion present in that image is another important reason behind achieving better performance in the proposed work.

6 Conclusion

The proposed work develops an automated complete PASI scoring system for the assessment of psoriasis from raw 2D and RGB colour images of the body regions of patients. It is fully automated as it is based on a DL framework and doesn't rely on hand-crafted features. This will be beneficial for dermatologists by providing an objective way for automatic estimation of different parameters of PASI i.e., psoriasis area (A) and clinical severity (R, S, and T) scores. In the proposed system, the segmentation task is performed using a UNet model with the MobileNetV2 network as a backbone. The severity classification task is carried out on each segmented lesion by a hybrid model having the fused strengths of both local and global processing from MobileNetV2 and ViT, respectively. The exhaustive experimental analysis with five-fold cross-validation is performed and different performance metrics are evaluated to show the adequacy of the proposed system. On the test dataset, the segmentation model in the proposed system achieves 0.0400MAE for psoriasis area scoring with an ICC of 0.9630. The proposed classification model developed for redness, scaliness, and thickness severity scoring achieves MAE of 0.2314, 0.2200, and 0.2086 with ICC of 0.7806, 0.8024, and 0.8205 respectively. However, the overall proposed system achieves MAE and ICC of 1.0200 and 0.9100, respectively for the objective calculation of the PASI score. However, these performances are getting further improved on the inclusion of ± 1 score tolerance limit such as MAE becomes 0.0571 for R, 0.0285 for S, 0.0171 for T, 0.0000 for A, and 0.8029 for PASI. These results of the proposed system are found outstanding when compared with other different fully automated approaches from the literature.

Thus, the proposed *PASI* scoring system has the potential to avoid the tedious and manual calculation of *PASI* in routine mode. It also offers quantitative and reproducible diagnosis and assessment for psoriasis treatment. Thus, it can easily be adaptable in large psoriasis research or clinical studies such as drug evaluation and therapy, etc. for psoriasis treatment. Also, the lightweight models used in the proposed system are mobile-friendly and they can be used by the concerned to monitor the disease severity remotely with ease.

The fusion of features from multi-scale and multi-view inputs with self-supervised DL models can be explored and incorporated in the future to improve the performance of automatic severity assessment of psoriasis lesions. Further, a better and more generalized *PASI* scoring system may be developed by utilizing a large psoriasis image dataset of multiple skin types annotated by multiple experts. **Acknowledgements** We thank all the dermatologists and psoriasis patients of Psoriasis Clinic and Research Centre, Psoriatreat, Pune, Maharashtra, India who are involved in this research.

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Declarations

Competing interests The authors have no competing interests to declare that are relevant to the content of this article.

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